

Abstract:

Applying Field Programmable Gate Arrays to Biological Problems;

Today's vast amount of biology-genomic data is growing beyond the researcher's ability to analyze it in a reasonable amount of time. In this paper, we will show how a Field Programmable Gate Array (FPGA) can be applied in biological problems to increase computational speed.

FPGAs are Large Scale Integrated circuits made up of programmable logic which can perform the functionality of basic logic gates such as AND, OR, XOR, and NOT, or complex combinatorial functions such as decoders and adders. This logic can be re-configured by the user to implement computationally extensive algorithms in. Since FPGAs are inherently parallel devices, they can offload from the main processor these high computation steps and accelerate them in hardware thus reducing the main processors overhead. In addition to programmed custom calculations done in hardware, the FPGA can take advantage of data level parallelism where a single pipeline inside the FPGA can spilt the data across multiple pipelines to help attain the required speedup.

Biological applications that require high data throughput such as pattern matching, multiple sequence alignment, structural genomics, protein-ligand binding and gene sequencing can take advantage of the parallel exploitation provided by using FPGAs and impact current research by reducing the time it takes to analyze the data. This paper will give a brief outline of how FPGAs can be applied to computational biological problems and what FPGA tools are currently available to researchers in the life sciences field. The author's will relate their experiences in using FPGAs in this application domain.